abl gene. Homo Lung cancer associ

ALIGNMENTS

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AC
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KW
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OS
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PR
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PT
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        Homo sapiens.
        WO9314193-A.
         22-JUL-1993.
                             93WO-US000445.
         05-JAN-1993;
                               92US-0820011.
         06-JAN-1992;
         (UYYA ) UNIV YALE.
         Bell L. Luthringer DJ, Madri JA, Warren SL;
         WPI; 1993-243209/30.
P-PSDB; AAR39705.
          Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced mononuclear cell adhesion and fibronectin prodn
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Disclosure; Page 69-72; 91pp; English.

The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide is used to transform endothelial cells. Transformed cells produce increased amounts of pp60 c-src and have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced mononuclear cell adhesion. They can also be used to improve the success of surgical procedures such as coronary angioplasty, heart bypass surgery, vessel graft and stent implantation.

Sequence 1611 BP; 334 A; 507 C; 504 G; 266 T; 0 other;

Оу	D dy	Оy	P Qy	Db Qy	g Q	₽.	Од	gb Qy	Qy Db	Qy Db	DB VQY	Qy dd	ery Match
721 tgccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaag 780	661 acccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctg 720 	601 aacgtgaagcactacaagatccgcaagctggacagcggcggcttctacatcacctcccgc 660 	541 gagaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctc 600	481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540 	421 gcgccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggag 480 	361 tggtggctggcccactcgctcagcacaggacagacaggctacatccccágcaactacgtg 420	301 acagacetgteetteaagaaaggegageggeteeagattgteaacaacaeggagggagae 360 	241 ccgctggccggtggagtgaccacctttgtggccctctatgactatgagtctaggacggag 300 	181 cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagagggcgggc	121 ccagcctcggccgacggccaccgcggccccagcgcggccttcgcccccgcggccgccgag 180	61 gccyagaacytycacygcyctygcygygycyctttccccycctcycagacccccagcaag 120 	1 atgggtagcaacaagagcaagcccaaggatgccagccgcagcggcgccgcagcctggagccc 60	y Match 99.9%; Score 1609.4; DB 14; Length 1611; Local Similarity 99.9%; Pred. No. 2.9e-294; hes 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT

ALIGNMENTS

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US-07-820-011A-3
; Sequence 3, Application US/07820011A
; Patent No. 5336615
; GENERAL INFORMATION:
   APPLICANT: Bell, Leonard
   APPLICANT: Madri, Joseph A.
   APPLICANT: Warren, Stephen L.
   APPLICANT: Luthringer, Daniel J.
   APPLICANT: Luthringer, Daniel J.
   TITLE OF INVENTION: Genetically Engineered
   TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
   TITLE OF INVENTION: Migration
   TOOPTION TO SEED (Migration Migration)
   TOOPTION: Migration
   TITLE OF INVENTION: Migration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nuclectide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: the Carboxy-Terminal Two-Thirds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 1610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.9%; Score 1609.4; Best Local Similarity 99.9%; Pred. No. 0;
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                                                                                              421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSUE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL:
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Gibbs, Carol P.
Arthur, Richard R.
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us-09-44

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                        06-JAN-1992;
                        (UYYA ) UNIV YALE.
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                        Bell L, Luthringer DJ, Madri JA, Warren SL;
                        WPI; 1993-243209/30.
DR
                        P-PSDB; AAR39705.
               DR
                        Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced mononuclear cell adhesion and fibronectin prodn
               Disclosure; Page 75-77; 91pp; English.
                        The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in AAQ46688) is used to transform endothelial cells. Transformed cells produce increased amounts of pp60 c-src and have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced mononuclear cell adhesion. They can also be used to improve the success of surgical procedures such as coronary angioplasty, heart bypass surgery, vessel graft and stent implantation.
                         implantation.
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                                         seq_documentation_block:
                                                Sequence 4, Application US/07820011A
Patent No. 5336615
                                                    Patent No. 5336615

GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration,
TITLE OF INVENTION: and Plasminogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
CORRESPONDENCE ADDRESS: ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairifield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Riee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEFAX: (203) 255 1400
TELEFAX: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: AMINO ACID
TOPOLOGY: Linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
FRAGMENT TYPE: Complete Sequence
ORGANISM: Homo sapien
PUBLICATION INFORMATION:
                                                                 CORRESPONDENCE ADDRESS:
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                                                                     ORGANISM: Homo sapien
PUBLICATION INFORMATION:
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AUTHORS: Anderson, Stephen K.
AUTHORS: Gibbs, Carol P.
AUTHORS: Tanaka, Akio
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: Human Cellular src Gene:
TITLE: Nucleotide Sequence and Derived Amino
TITLE: Acid Sequence of the Region Coding for
TITLE: pb60c-src
     12
                                                                                                               pp60c-src
                                                                                JOURNAL: Molecular and Cellular Biology VOLUME: 5
                                                                        PAGES: 1122-1129
DATE: May, 1985
PUBLICATION INFORMATION:
                                                                                AUTHORS: Tanaka, Akio
AUTHORS: Gibbs, Carol P.
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Page 2

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US-09-444-711-1 x US-07-820-011A-4
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Ratio: 5.287
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Anderson, Stephen K.
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	1351 TTCGGGATCCT	1301 CAGAAGCTGCC 434 roGluAlaAla	1251 TGAGTACACGG 17 nGluTyrThra	1201 CTGGTGTGCAAA 	1151 ACTACGTCCAC	1101 GGACATGGCT 367 laspMetala	1051 GACTTTCTCAAG 11	1001 AGGAGCCCAT	951 GAAGAAGCTGA 317 tLysLysLeuA	901 AAGCCTGGCA 301 LysProGlyT	851 TGTGGATGGG 1 284 altrpMetGl	801 GGAGTCGCTG 267 gGluSerLeu	751 TCCAAGCCGC 251 SerLysProg		651 CACCTCCCG 217 eThrSerAr	601 AACGTGAAG 201 AsnValLys	4
uLeuThrGluLeuThrThrLysGlyArgValPr	CTGACTGAGCTCACCACAAAGCCCACGCCTCC	CTCTATGGCCGCTTCACCATCAAGTCGGACGTG 	CGCGGCAAGGTGCCAAATTCCCCATCAAGTGGA 	GTGGCCGACTTTGGGCTGGCTCGCCTCATTG 	CGGGACCTTCGTGCAGCCAACATCCTGGTGGG 	CGTGGAG ValGlu	AGGGGGAGACAGGCAAGTACCTGCGGCTGCCTC 	TTACATCGTCACGGAGTACATGAGCAAGGGGAG 	AGGCATGAGAAGCTGGTGCAGTTGTATGCTGTG 	CGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCC 	GACCTGGAACGGTACCACCAGGGTGGCCATCAAA 	CGGCTGGAGGTCAAGCTGGGCCAGGCTGCTTT 	AGACTCAGGGCCTGGCCAAGGATGCCTGGGAGA 	CGATGGCCTGTGCCACCGCCTCACCACCGTGT 	CACCCAGTTCAACAGCCTGCAGCAGCTGGTGGC 	CACTACAAGATCCGCAAGCTGGACAGCGGCGGC 	yrCysLeuSerValSerAspPheAspAsnAlaLy
OTYrPr 467		TGGTCC 1350 TrpSer 450	ACGGCTC 1300 hrAlap 434	AAGACAA 1250 uAspas 417	AGAGAAC 1200 YGluAsn 400	CGGATGA 1150 ArgMeta 384	AGCTGGT 1100 nLeuva 367	TTTGCTG 1050	GTTTCAG 1000 ValserG 334	AGGTCAT 950	AACCCTG 900 sThrLeu 300	RGGCGAGG 850 GlyGluV 284	ATCCCTCG 800	GCCCCACG 750 ysProThr 250	CTACTACT 700 aTyrTyrS 234	TTCTACAT 650 PheTyrIl 217	ysGlyLeu 200

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1601 AGAACCTC 1608 ||||||| 534 luAsnLeu 536

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Genetically engineered endothelial cells - which exhibit e	WPI; 1993-243209/30. P-PSDB; AAR39705.	Bell L, Luthringer DJ, Madri JA, Warren SL;	(UYYA) UNIV YALE.	06-JAN-1992; 92US-0820011.	00 0000 ±000; 0000 000000#40.	05-Tan-1993: 93W0-#6000445	22-JUL-1993.		W09314193-A.	Homo sapiens.	,	Endothelial; tyrosine kinase protein; pp60 c-src; ss.	Human pp60 c-src gene.		23-DEC-1993 (first entry)		AAO46688:	AAQ46688 Standard; cDNA to mRNA; 1611 BP.	

Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced mononuclear cell adhesion and fibronectin prodn

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; PAGES: 1978-1983
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: Fujita, Donald J.
DNA Sequence Encoding the
Amino-Terminal Region of the Human c-src
Protein: Implications of Sequence
Divergence among src-Type Kinase
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	GAGTRACACGGGGGGGAAGGTGCCAAATTCCCCATCAAGT	CTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTG	ACTTTCTCAAGGGGAGACAGGCAAGTACCTGCGGCTGCC	AAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTG	GTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATC		CAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGCGTG	SGlyAlaTyrCysLeuSerValSerAspPheAspAsnAla ACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGG
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polymcleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC diagnostic coding sequences of the invention.
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC art for winn introducts obtained in electronic format directly from WIPO

of the polyperide and polynucleotide is equenced to the printed
CC amino acid sequences obtained in electronic format directly from WIPO

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GENERAL INFORMATION:
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                                                                        APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically
TITLE OF INVENTION: Endothelial
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                                     CORRESPONDENCE ADDRESS
                                                                                                                                                        APPLICANT:
                                                           NUMBER OF SEQUENCES:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
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alignment_scores:
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Quality: 2834.00
Ratio: 5.287
Percent Similarity: 100.000
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DATE: MAY, 1985
PUBLICATION INFORMATION:
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APPLICATION NUMBER: 07/820,011
FILING DATE: 06-JAN-1992
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ORIGINAL SOURCE:
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MEDIUM TYPE: 3.5 inc
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NAME: Klee, Maurice M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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OPERATING SYSTEM: DOS 5.0
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TYPE: AMINO ACID
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REFERENCE/DOCKET NUMBER: ALX-101PCT
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: Fujita, Donald J.
Human Cellular src Gene:
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                                                                                                                                                                                                                                                                                                                           Tanaka, Akio
Gibbs, Carol P.
Arthur, Richard R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibbs, Carol
Tanaka, Akio
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                                                                                                                                                                                                                                                                                           Anderson, Stephen K.
Kung, Hsing-Jien
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                                                                                                                                                                   Modulating vascular permeability in tissues, including tissues associated with stroke, myocardial infarction, the tissue with tyrosine kinase protein Src, Yes or the
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             The specification describes a method for modulating vascular permeability in a tissue suffering from a disease condition. The method
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                                                                                                   Disclosure;
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29-MAR-2000; 2000US-0538248.
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No. 1.4e-220;
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D; Mismatches 229;
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RESULT 5
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PCT-US93-06251-83
Sequence 83, Application PC
GENERAL INFORMATION:
APPLICANT: Wickstrom,
APPLICANT: OF INVENTION: T)
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NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 6886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEEX: 230 901 SANS UR
                                                                                                                                                                                                  COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                            APPLICATION NUMBER: PCT/N FILING DATE: 19930630 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: DiGiglio, Frank S.
                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                        CITY:
STATE:
                                                                                                                                                                                                                                                                                   ADDRESSEE: SCULLY, SCOTT, MURPHY STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                            gactacttcacgtccaccgagccccagtaccagcccggggagaacctctag
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WENTION: Trivalent Synthesis of Oligonucleotides Containing
WENTION: Stereospecific Alkylphosphonates and Arylphosphona
EQUENCES: 93
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The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                         polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
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Best Local Similarity
Matches 1029; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a
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alignment_block: alignment_scores: Quality: 2408.50 Ratio: 4.946 Percent Similarity: 88.545 US-09-444-711-1 x ABG23778 gn seg 1/1 to: ABG23778 116 GluArgLeuGlnIleValAsnAsnThrLysGlyAspTrpTrpLeuAlaHi disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO 575 182 525 166 475 149 425 132 375 625 199 275 TCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGC 324 225 CCCGCAGAGGGCGGGCCGGCTGGCCGGTGACCACCTTTGTGGCCC 274 193 GGAGGCTTCAACTCCTCGGACACC......GTCACCTC 22 143 GCGGCCCAGCGCGCTTCGCCCCCGCGGCCGAGCCCAAGCTGTTC 192 103TCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACC 142 Sequence 99 82 lProArgTyrLysLeuThrCysThrGlyGlyValThrThrPheValAlaL 66 49 32 gargLeuHisSerPheThrGlnThrArgSerLeuSerProGlnAlaHisA at ftp.wipo.int/pub/published_pct_sequences. 16 ProGluArgAlaValLeuGluSerArgGlyGlyAlaProAspThrProAr 32 CCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGA 474 GlyGlyGlyArgValThrAspThrArgArgHisIleProAsnAlaAspVa 82 laGlyProHisThrArgLeuHisProArgGlnGlyHisAlaHisMetArg 65 AAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCAACAG CTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGATCCGC CGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTT 524 CCCGCCGAGAACGTGCACGGCGCTGGCGGGGGGGGCGCTTTCCCCGGCC.... 102 565 AA; from: 1 Percent Identity: 85.273 to: 565 674 215 624 199 574 182 132 49 99

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1308 465	9 CGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCT 	125
1258 449	9 CAAAGTGGCCGACTTTGGGCTGGCTCGGCTCATTGAAGACAATGAGTACA 	120
1208 432	9 CACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTG	115 41
1158 415	9 CTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTC 	110 39
1108 399	9 CAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGTGGACATGG 	105 38
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1008 365	9 TGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCC 	as on
958 349	9 CACGATGTCTCCAGAGGCCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGC	90 33
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858 315	9 TGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATG 	80 29
808 299	9 GCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGC 	75 28
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The specification describes a method for modulating vascular permeability in a tissue suffering from a disease condition. The method cc comprises contacting the tissue with a pharmaceutical composition comprises the present of the method is useful for modulating comprises or contacting them. The method is useful for modulating composition contacting them the method is useful for modulating composition contacting the process of the contacting them the method is useful for modulating composition contacting the process of the contacting them the method influence of contacting them to blood vessels, and other systemic pathological events such as atherosclerosis, diabetic retinopathy, inflammatory disease due to infection by microbial agents and arthritis. Other diseases which can be treated include adult respiratory distress syndrome (ARDS), rheumatoid carefullary proliferation in atherosclerotic plaques and osteoporosis and cancer associated disorders such as solid tumours, solid tumour contacting the method of the treated includes and is used in the method of the treated in the contaction of the present sequence.

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normal flow, tissues undergoing restenosis, psoriatic, retinal tissue and similar tissues. Pathologies which may be treated include include trauma to blood vessels, and other systemic pathological events such as atherosclerosis, diabetic retinopathy, inflammatory disease due to infection by microbial agents and arthritis. Other diseases which can be treated include adult respiratory distress syntoreme (ARDS), rheumatoid arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma, capillary proliferation in atherosclerotic plaques and osteoporosis and cancer associated disorders such as solid tumours, solid tumour metastases, angiofibromas and hemangiomas. The present sequence represents human Yes, and is used in the method of the invention. nucleic acid expressing them. The method is useful for modulating vascular permeability in tissues, including inflamed tissue, tissues associated with stroke, myocardial infarction or other blockage of permeability in a tissue suffering from a disease condition. The comprises contacting the tissue with a pharmaceutical composition comprising tyrosine kinase protein Src, Yes or their mixtures or the mixtures or their mixtures or the mixtures of the mixtures or the mixtures of the mixtures or the mixtures or the mixt The specification describes a method for modulating vascular method

Sequence 543 A,

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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifty. Wipo.int/pub/published_pct_sequences.
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alignment_scores:
Quality: 2115.50
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Percent Similarity: 86.630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention. The cellular immunogen of the invention is for immunising against the product of a target proto-oncogene, over-expression of which
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Anticancer composition comprising two anti-sense oligo:nucleotide(s)

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Search completed: June 4, 2002, 09:36:41 Job time: 4213 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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  Issued_Patents_NA:*
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Copyright (c) 1993 - 2000 Com
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7302.373 Million cell updates/sec
            US-08-306-691B-35
US-09-328-111-821
US-08-604-989A-9
US-08-604-989A-10
US-08-604-989A-11
US-08-426-509A-1
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US-09-228-603A-1

US-09-173-581-12

US-09-420-915-12

US-09-006-675-7

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US-08-426-509A-5
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PCT-US93-06251-66
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                 Sequence 12, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 19, Appli
Sequence 19, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 35, Appl
Sequence 821, Appl
Sequence 821, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence 1, Appli
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Sequence 83, Appl
Sequence 77, Appl
Sequence 40, Appl
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US-07-820-011A-3
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APPLICANT:
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161	161	162.6	162.6	162.6	165	165	170.4	181.2	182	182	200	203.4	207.6	207.6	207.6	210.8	210.8
10.0	10.0	10.1	10.1	10.1	10.2	10.2	10.6	11.2	11.3	11.3	12.4	12.6	12.9	12.9	12.9	13.1	13.1
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US-08-162-809-11	US-08-162-809-17	PCT-US95-04681-10	US-08-702-367A-10	US-08-449-645A-10	US-08-162-809-13	US-08-162-809-9	US-09-817-180-1	US-08-391-615-1	PCT-US93-06251-72	US-08-306-691B-30	US-08-876-882-1	US-09-142-529-2	PCT-US95-05008-3	US-08-426-509A-3	US-08-604-989A-8	PCT-US93-06251-76	US-08-306-691B-34
Sequence 11, Appl	Sequence 17, Appl		10,	10,	13	ė	μ.	Sequence 1, Appli		Sequence 30, Appl	۲,	2	ω	Sequence 3, Appli	Sequence 8, Appli	Sequence 76, Appl	Sequence 34, Appl

ALIGNMENTS

Madri, Joseph A. Warren, Stephen L. Bell, Leonard

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APPLICATION NUMBER: US/07/820
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
                                                                                                                                                                                    TELEFAX: (203) 254 110 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                               MOLECULE TYPE: OHYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: 5.25 in
COMPUTER: IBM PC XT
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: LB TELECOMMUNICATION INFORMATION: TELEPHONE: (203) 255 1400
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Displaywrite 3 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                   LENGTH: 1611
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                 ORGANISM:
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OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
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CITY: Fairifield
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                               Homo sapien
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                                                                                                   cDNA to mRNA
                                                                                                                                    Double
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3:
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Chromosome
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RESULT 2
PCT-US93-00445-3
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ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-101PCT
FELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application PC/TUS9300445 GENERAL INFORMATION:
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MEDIUM TYPE: 3.5 inch, 760 Kb storag.
COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00445
FILING DATE: 19930105
                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CD
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ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: C
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LENGTH: 1611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Genetically EngineTITLE OF INVENTION: Endothelial Cells NUMBER OF SEQUENCES: 4
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                                                  DATE: May, 1985
PUBLICATION INFORMATION:
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                                                                                                                                                                                                              AUTHORS:
TITLE: H
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CITY: Fairfield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                AUTHORS:
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                                                                                                                                                        Nucleotide Sequence and Derived Amino
Acid Sequence of the Region Coding for
the Carboxy-Terminal Two-Thirds of
pp60c-src
                                                                                                                                                                                                                          : Kung, Hsing-Jien
: Fujita, Donald J.
Human Cellular src Gene:
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NVENTION: Genetically Engineered
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Tanaka, Akio
Gibbs, Carol P.
Arthur, Richard R.
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Warren, Stephen L.
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DATE: May, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
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RESULT 4
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ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEPAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
TYPE: NUCLEIC ACID
STEADSTONESS: DOLLDIST
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APPLICANT:
APPLICANT:
                                                                                                                           ORGANISM: Gallus, gallus PUBLICATION INFORMATION: AUTHORS: Takeya, Tatsuo
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically
TITLE OF INVENTION: Endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 19
                                                    AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to th
TITLE: Gene and the Mechanism for Gen
TITLE: Transforming Virus
                                                                                                                                                                                                                                   TOPOLOGY: Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 19930
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1951 Burr Street
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Best Local S
Matches 955
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
CT-US93-06251-83
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TTCCACAGCTGGTTGATATGGCTGCTCAGATTGCTGATGGTATGGCATATATTGAAAGAA
                    tgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggagcgga
                                                                       acatgagcaagggagtttgctggactttctcaagggggagacaggcaagtacctgcggc
                                                                                                                            agaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcgtcacggagt
                                                                                                                                                                  GTACAATGATGCCAGAAGCTTTCCTTCAAGAAGCTCAGATAATGAAAAAATTAAGACATG
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                                                        ATAAACTTGTTCCACTATATGCTGTTGTTTCTGAAGAACCAATTTACATTGTCACTGAAT
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Pred. No. 2.2e-135;
0; Mismatches 408;
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PCT-US93-06251-77; Sequence 77, Application PC/TUS9306251; GENERAL INFORMATION:
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                                                                                  TELEFAX: 516-742-4366
TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC: compartible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: D1G1g110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1796
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2647 base pair
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   MOLECULE TYPE:
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               STRANDEDNESS:
TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                           H: 2647 base pairs nucleic acid
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DNA (genomic)
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                             ATGAATCTGTGTTGGAAGAAGGACCCTGATGAAAGACCATCTGAATATGTTCAGTCC
                                                  atgtgccagtgctggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggcc 1551
                                                                                                                                                          ctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcgaggtgctggaccag
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PCT-US93-06251-82
Sequence 82, Applicat
GENERAL INFORMATION:
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PCT-US93-06251-82
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Best Local S
Matches 742
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SEQUENCE CHARACTERISTICS:
LENGTH: 1804 base pairs
TYPE: nucleic acid
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TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphona
NUMBER OF SEQUENCES: 93
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nes 742; Conserv
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CLASSIFICATION:
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Pred. No. 5.7
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Weinstein, Daniel C.
TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESSONDENCE ADDRESS:
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CITY: Hackensack
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 APPLICATION NUMBER:
                                                                                                                COUNTRY: UZIP: 07601
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                                                                                                                                              New Jersey
                                                                                                                                                                              411 Hackensack Avenue,
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Best Local Similarity
Matches 822; Conserv
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 600-1-217
TELECOMMUNICATION INFORMATION:
TELEPAN: 201-343-160'
TELEPAN: 201-343-160'
TELEYAN: 201-343-160'
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ATTORNEY/AGENT INFORMATION:
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Pred. No. 5:2e-86;
0; Mismatches 492;
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RESULT 13
US-09-006-675-7
; Sequence 7, Application US/09006675
; Patent No. 5952213
; GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-10-20
EEARLIER APPLICATION NUMBER: US 09/173,581
EEARLIER FILING DATE: 1998-10-15
NUMBER OF SEO ID NOS: 18
SOFTWARE: PERL Program
SEO ID NO 12
LENGTH: 1574
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OTHER INFORMATION: 507669
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ORGANISM: Homo sapiens
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Pred. No. 8.5e-62;
0; Mismatches 198;
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; LOCATION:
US-09-006-675-7
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Best Local Similarity 65.8%;
Matches 513; Conservative
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1144 cggatgaactacgtccaccgggaccttcgtgcagccaacatcctggtgggagagaacctt
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                           1024
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LENGTH: 780 base pairs
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 12
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TELEFAX: 133521
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REFERENCE/DOCKET NUMBER: 600-
SLECOMMUNICATION INFORMATION TREASURED NAME AND ADDRESS OF TRANSPORT NAME AND ADDRESS OF TREASURED NAME AND ADDRESS OF TRANSPORT NAME AND ADDRESS OF TRANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 411 Hacke
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tgggagatccctcgggagtcgctgcggctggaggtcaagctgggccagggctgcttttggc 846
                                                                                                                                            cggctgcctcagctggtggacatggctgctcagatcgcctcaggcatggcgtacgtggag 1143
                                                                                                                                                                                                                                                                            GATGTTTGGTTGGCCATGTACAATGGACACACAAAAGTAGCTGTAAAAAACAATGAAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGGAGATCCCGCGCGAGTCACTGTCACTGCAGAAGAAGCTTGGAGCTGGACAGTTTGGG 60
                                                                                                   CCTCTGATTCAACTCATTGACTTCTCTGCCCAGATTGCAGAAGGAATGTGGTTTATTGAG
                                                                                                                                                                                                                                  GAGTATATGCAAAAGGGCAGTTTGCTGGATTTCCTGAAAAGTGAAGAAGGTAGCGACCAA 300
                                                                                                                                                                                                                                                                                                                                                                     gagaagctggtgcagttgtatgc---tgtggtttcagaggagcccatttacatcgtcacg 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAGCATGTCCCCCGGTGCCTTCCTTGAAGAGGCAAATCTGATGAAGAGCTTGCAGCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagctgaggcat 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccctgaagcct 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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Pred. No. 6.4e-61;
0; Mismatches 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600-1-217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          780;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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TOPOLOGY: US-08-426-509A-5
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Best Local Similarity 54.1%;
Matches 730; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2770 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEND VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILLING DATE: 21-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                               848
968 TGTCAAGCTGGGGAAACCATGCTTAAAGATCCAGGTCCCAGCTCCATTTGATTTGTCGTA 1027
                                                                                                       908
                                                                                                                                                                                                                                              603
                                                                                                                                                                                                                                                                                  803 AAGCCAAAAAGGAGAATTCTCTCTTTCAGTTTTAG------ATGGAGCAGT 847
                                                                                                                                                                                                                                                                                                                                                                                                                                      483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        623 GAAAAGACGAGATGGCTCCAGTCAGCAACTACAAGGCTATATTCCTTCTAACTACGTGGC 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 TGACAAACTTCAAGTTCTGGACACTTTGCATGAGGGCTGGTGGTTTGCCAGACACTTGGA 622
                                                                                                                                                                                                                                                                                                           543 gaccacgaaaggtgcctactgcctctcagtgtctgacttcgacaacgccaagggcctcaa 602
                                                                                                                                                                                                                                                                                                                                                                                         743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          683 TGAGGACAGAAGCCTACAGGCAGAGCCGTGGTTCTTTGGAGCAATCGGAAGATCAGATGC 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 gccctccgactccatccaggctgaggagtggtattttggcaagatcaccagacgggagtc 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 ctttgtggccctctatgactatgagtctaggacggagacaggacctgtccttcaagaaagg 323
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                                         ccaccgcctcaccacgtgtgccccacgtccaagccgcagactc-----aggg 770
                                                                                                                                    ccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcctgtg
                                                                                                                                                                                     TGTAAAACACTACAGAATTAAAAGACTGGATGAAGGGGGATTTTTTCTCACGCGAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                           agagoggttactgotcaatgcagagagacccgagagggaccttcctcgtgogagaaagtga 542
                                                                                             AATCTTTTCAACACTGAACGAATTTGTGAGCCACTACACCAAGACAAGTGACGGCCTGTG
                                                                                                                                                                                                                     cytyaaycactacaayatccycaayctyyacaycygcttctacatcacctcccycac 662
                                                                                                                                                                                                                                                                                                                                                                                AGAGAAACAACTATTATATTCAGAAAACAAGACCGGTTCCTTTCTAATCAGAGAAAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTGTGGCTTTGTTTGATTACCAGGCTCGGACTGCTGAGGACTTGAGCTTCCGAGCAGG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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	1539 gtacctgcaggccttcctggaggactactt 1568	Qy
A 1807	NACATCATGTTGGAGTGCTGGAATGCAGAGCCTAAGGAACGACCTACATTTG	Db
ja 153	1479 cctgcacgacctcatgtgccagtgctggcggaaggagcctgaggagcggcccaccttcg	Qy
:A 1747	rccagatéttégeteaaaactatagaetteegeaaceatecaacteree	Db
c 147	1419 ggtgctggaccaggtggagcgggggctaccggatgccctgcccgccc	Qy
'A 168	1628 CCTTCTTTATGAAATCATTACTTATGGCAAAATGCCTTACAGTGGTATGACAGGTGCCCA	뫄
a 1418	1359 cctgctgactgagctcaccacaaagggacgggtgccctaccctgggatggtgaaccgcga	Qy
T 1627	1568 GCCCGAAGCCATTCGTAGTAATAAATTCAGCATTAAGTCCGATGTATGGTCATTTGGAAT	Ф
ıt 135	1299 tccagaagctgccctctatggccgcttcaccatcaagtcggacgtgtggtccttcggga	Qy
C 1567	1508 AGATAATGAAGACATCTATGAATCTAGACACGAAATAAAGCTGCCGGTGAAGTGGACTGC	ф
rc 1298	1248 caatgagtacacggcgcgggcaaggtgccaaattccccatcaagtggacgg	Qy
T 1507	1448 CGTTGGTGAACATAATATCTACAAAGTAGCAGATTTTGGACTTGCCAGAGTTTTTAAGGT	Дb
ja 1247	1188 ggtgggagaacctggtgtgcaaagtggccgactttgggctggct	Qy
T 1447	1388 AATGGCCTATCTGGAGTCTCGGAACTACATTCACAGAGATCTGGCTGCCAGAAATGTCCT	DЬ
t 1187	1128 catggcgtacgtggagcggatgaactacgtccaccgggaccttcgtgcagccaacatcc	Qy.
G 1387	1328 CACTGGATCAAAAATCCATCTGACTCAACAGGTAGACATGGCGGCACAGGTTGCCTCTGG	Db
yg 1127	1068 gacaggcaagtacctgcggctgcctcagctggtggacatggctgctcagatcgcctcag	Qy
3A 1327	1268 AATTTATATTACAGAGTTGATGAGACATGGAAGTCTGCAAGAATGTCTCCCAAAATGA	망
ya 106	1008 catttacatcgtcacggagtacatgagcaaggggagtttgctggactttctcaaggggg	Qy
C 1267	1208 GAAGAACCTAAGACATCCAAAGCTTATCCAGCTTTATGCTGTTTGCACTTTAGAAGATCC	DЬ
c 1007	951 gaagaagctgaggcatgagaagctggtgcagttgtatgctgtggtttcagaggagc	Qy
AT 1207	1148 GAAAACATTAAAACCAGGTTCAATGGATCCAAATGACTTCCTGAGGGAGG	Db
at 950	octgaagcctggcacgatgtctccagaggccttcctgcaggagg	Qy
 3T 1147	CAGTTTGGCGAAGTATGGGAAGGTCTGTGGAACAATACCACTCCAGTAGCAG	Db
at 890	831 ccagggctgctttggcgaggtgtggatgggacctggaacggtaccaccagggtggcca	Qy
3G 1087	1028 TAAAACCGTGGACCAATGGGAGATAGACCGCAACTCCATACAGCTTCTGAAGCGATTGGG	В
yg 830	771 cctggccaaggatgcctgggagatccctcgggagtcgctgcggctggaggtcaagctgg	Qy

Search completed: June 4, 2002, 09:32:35 Job time: 3967 sec

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/5B_COMB.pep:US-07-857-224B-51 +

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/cgn2_6/ptodata/1/laa/5B_COMB.pep:US-09-006-675-2 + 1441.00 1722.18 3.8e/cgn2_6/ptodata/1/laa/6B_COMB.pep:US-09-28-6033-2 + 1441.00 1722.18 3.8e/cgn2_6/ptodata/1/laa/6B_COMB.pep:US-08-426-5093-19 + 1439.50 1720.32 4.8e/cgn2_6/ptodata/1/laa/6B_COMB.pep:US-08-195-05008-19 + 1439.50 1720.32 4.8e/cgn2_6/ptodata/1/laa/5B_COMB.pep:PCT-US95-05008-19 + 1439.50 1720.32 4.8e/cgn2_6/ptodata/1/laa/5B_COMB.pep:US-08-318-9478-21 + 1252.50 1642.02 2.1969.26/ptodata/1/laa/5B_COMB.pep:US-08-318-9478-21 + 1252.50 1502.53 1.3e/cgn2_6/ptodata/1/laa/5B_COMB.pep:US-08-795-303-21 + 1252.50 1502.53 1.3e/cgn2_6/ptodata/1/laa/5B_COMB.pep:US-08-7857-224B-50 + 1246.00 1492.60 5.9e/cgn2_6/ptodata/1/laa/5B_COMB.pep:US-09-395-7841-4 + 1228.00 1472.60 5.9e/cgn2_6/ptodata/1/laa/5B_COMB.pep:US-09-395-841-4 + 1228.00 1472.60 5.9e/cgn2_6/ptodata/1/laa/6B_COMB.pep:US-09-390-455-4 + 1228.00 1472.60 5.9e/cgn2_6/ptodata/
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Database sequences: 231628
Database length: 24425594
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6/ptodata/1/laa/6B_COMB.pep:US-08-426-509A-11 + 1932.50 2312.37 4.7e-122
6/ptodata/1/laa/PCTUS_COMB.pep:PCT-US95-05008-11 + 1932.50 2312.37 4.7e-12
6/ptodata/1/laa/PCTUS_COMB.pep:PCT-US95-05008-11 + 1932.50 2312.37 4.7e-11
6/gn2_6/ptodata/1/laa/PCTUS_COMB.pep:US-08-426-509A-17 + 1529.00 1827.81 4.9e-95
6/ptodata/1/laa/6B_COMB.pep:US-08-426-509A-17 + 1529.00 1827.81 4.9e-95
6/gn2_6/ptodata/1/laa/ACTUS_COMB.pep:PCT-US95-05008-17 + 1529.00 1827.81 4.9e-95
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:US-08-955B-17 + 1464.00 1749.58 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:US-08-426-509A-18 + 1464.00 1749.58 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:US-08-426-509A-18 + 1464.00 1749.58 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:US-08-426-509A-16 + 1464.00 1749.58 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:US-08-426-509A-16 + 1464.00 1749.58 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:DCT-US95-05008-16 + 1464.00 1749.52 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:DCT-US95-05008-16 + 1464.00 1749.52 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:US-08-426-509A-16 + 1464.00 1749.52 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:DCT-US95-05008-16 + 1464.00 1749.52 1.1e-90
6/gn2_6/ptodata/1/laa/ACB_COMB.pep:US-08-426-509A-16 + 1464.00 1749.52 1.1e-90
6/gn2_6/ptodata/1
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/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:US-08-426-5-09A-16 + 1464.00 1749.52
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:US-08-95-05008-16 + 1464.00 1749.
/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:US-08-701-US95-05008-16 + 1464.00 1749.
/cgn2_6/ptodata/1/1aa/SB_COMB.pep:US-08-701-US1A-32 + 1447.00 1735.29
/cgn2_6/ptodata/1/1aa/SB_COMB.pep:US-09-006-675-2 + 1441.00 1722.18 3
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cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-222-616-20 + 1;
cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:PCT-US95-04228-20
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-ARTRIX-blosum62 -TRANS-human40.cdi -LIST-45 -DOCALIGN-200
-ARTRIX-BORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-FMT-pfs -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-XR-US09444711_eCGN1_1_36 -NCPC-6 -TCPU-3 -LONGLOG
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seq_documentation_block:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 19920106
CLASSIFICATION: 435
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MEDIUM TYPE: 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: Anderson, Stephen
AUTHORS: Glbbs, Carol P.
AUTHORS: Tanaka, Akio
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NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                             AUTHORS:
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OPERATING SYSTEM: P
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Nucleotide Sequence and Derived Ami
Acid Sequence of the Region Coding
Acid Sequence of the Royal Two-Thirds of
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                                                                                                              Acid Sequence of the the Carboxy-Terminal
                                                                                                                                                                        Fujita, Donald J.
Human Cellular src Gene:
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INFORMATION:
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                                                                                 Molecular and Cellular Biology
                                                                                                                                                                                                           Kung, Hsing-Jien
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: Complete Sequence
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alignment_block:
US-09-444-711-1 x US-08-426-509A-13
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                                                                                 Quality: 2834.00
Ratio: 5.287
Percent Similarity: 100.000
Align seg 1/1
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                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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APPLICANT: Gishiz
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                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
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TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TITLE OF INVENTION: NOVEL M
TITLE OF INVENTION: TYROSIN
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
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REFERENCE/DOCKET NUMBER: 7683-0074-999
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Coruzzi, Laura A REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
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to: US-08-426-509A-13
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1155 Avenue of the Americas
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                                                          CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGCCGGCCCC
CAACTCCTCGGACACCGTCACCTCCCCGCAGAGGGCGGGGCCCGCTGGCCG
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seq_documentation_block:

Sequence 13, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.
APPLICANT: 515 Galveston Drive
APPLICANT: Redwood City, Californi

Sugen, Inc. 515 Galveston Drive Redwood City, Callfornia 94063-4720

seq_name: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US95-05008-13

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seg_documentation_block:
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APPLICANT: Bell,
APPLICANT: Madri,
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                                                                                                                                                                                                                                                                                                      APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanc
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity
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SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 19920106
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                        CITY: Fairifield
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5336615
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                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                             Maurice M. Klee
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                  US/07/820,011A
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alignment_block:
US-09-444-711-1 x US-07-820-011A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
ORGANISM: Gall
ORGANISM: Gallus, gallus PUBLICATION INFORMATION:
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                                                                                                                                                                                                    101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCACCGGCCCCC
                                                                                           301 ACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGATTGTCAACAACAC
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TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGES: 881-890
DATE: March, 1983
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Ratio: 5.107
milarity: 97.201
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AMINO ACID
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; PAGES: 881-890
; DATE: March, 1983
PCT-US93-00445-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: PCT-US93-00445-2
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AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
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TGGTATTTTGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAA 500
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Gaps: 1
Percent Identity: 93.843
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1 6	98	AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACAT 6	650
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2 7	'01 ?31	CCAAACACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACG .	750 247
2 7	'51 248	GGATGCCTGGGAGATCCCTCG 	800 264
N 60	01	GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 8 	850 281
2 8	151 181	TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 9 	900 297
2 9	01 98	AAGCCTGGCACGATGTCTCCAGAGGCCCTTCCTGCAGGAGGCCCAGGTCAT 9	950 314
ωυ)51 14	GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1 	1000
10 3	01 31	AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1 	1050
10 3	51 48	GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1 	1100
. 11	01	GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 1 	L150 381
11 3	51 81	ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 1	L200 397
12 3	98	CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTC	L250 114
12	51	TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCCATCAAGTGGACGGCTC 1 	131
13 4	01	CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1 	L350 147
13	51 48	TTCGGGATCCTGCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 1	L400 164
14	01	TGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGA 1 	450 81
14 4	51	TGCCCTGCCGGCGGAGTGTCCCGAGTCCTGCACGACCTCATGTGCCAG 1	.500

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US95-05008-14
                                                                                                                                                                                                                Sequence 14, Application PC/TUS9505008 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1521
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgAlaAlaAsnIleLeuValGlyGluAsnLeuValCysLysIleAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTCCACCGGGACCTT 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pGlyLysTyrLeuLysLeuProGlnLeuValAspMetAlaAlaGlnIleA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTC 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTGAGGCATGAGA 970
                                                                                                                                                                                                                                                                                                                                          hrAlaThrGluProGlnTyrGlnProGlyGluAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                         alLeuGluGlnValGluArgGlyTyrArgMetProCysProGlnGlyCys 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uLeuValThrLysGlyArgValProTyrProGlyMetValAsnArgGluV 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgPheThrIleLysSerAspValTrpSerPheGlyIleLeuGlnThrGl 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGA 1220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProGluSerLeuHisGluLeuMetAsnLeuCysTrpLysLysAspProAs 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugen, Inc.
515 Galveston Drive
Redwood City, California 94063-4720
United States of America
Wissenschaften E.V.
Hofgarten Str. 2
                                                                        Munchen 80539
            Kinases
                         Novel Megakaryocytic Protein Tyrosine
                                                                                                                                                                                                                                                                                                                                              543
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alignment_block: US-09-444-711-1 x PCT-US95-05008-14
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: PCT-US95-05008-14 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212)869-974:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZÍ, LAUTA A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/05008 FILING DATE: 24-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
271 GCCCTCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAA 320
                                                                              221 CCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTGACCACCTTTGTG 270
                                                                                                                                                                                                                                              142 CGCGGCCCAGCGGGCCTTCGCCCCGCGGCCGAGCCC..... 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                        17 gProGluAsnThrProGluProValSerThrSerValSerHisTyrGlyA
                                                                                                                                                                                                                                                                                                                                                                                                            48 CAGCCTGGAGCCCGCCGAGAACGTGCACGGCGCTGGCGGG......GGCG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGGGTAGCAACAAGAGCAAGCCC...AAGGATGCCAGCCAGCGGCGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetGlyCysIleLysSerLysGluAsnLysSerProAlaIleLysTyrAr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                    alProSerSerTyrProAlaGlyLeuThrGlyGlyValThrIlePheVal
                                                                                                                       ySerSerGlyValThrProPheGlyGlyAlaSerSerSerPheSerValV
                                                                                                                                                                                                        LysGlyThrAlaValAsnPheSerSerLeuSerMetThrProPheGlyGl
                                                                                                                                                                                                                                                                                       laGluProThrThrValSerProCysProSerSerSerAla.....
                                                                                                                                                                                                                                                                                                                               CTTTCCCCGCCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGCCAC 141
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(212)869-9741
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86.813
                                                                                                                                                             .AAGCTGTTCGGAGGCTTCAACTCCTCGGACACCGTCA 220
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O:
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12:

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alignment_block:

is=09-444-711-1 x US-08-426-509A-12
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Quality: 1949.00
Ratio: 4.350
Percent Similarity: 84.848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 536 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: No. 6326469
US-08-426-509A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jn seg 1/1 to:
                          481
                                                                                                                                                                                                                                                               381 CAGCACAGGACAGACAGGCTACATCCCCAGCAACTACGTGGCGCCCCTCCG 430
                                                                                                                                                                                                                                                                                                                                                                                     681 GCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTGTGCCACCGCC 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 AAGCTG...TTCGGAAGGCTTCAACTCCTCGGACACCGTCACCTCCCCGCA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 ACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGCGAGCGG 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 spTyrGluAlaArgThrGluAspAspLeuSerPheGlnLysGlyGluLys 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
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                                                                                                                                                                                                                       ProValProPheSerGlyProGlyPheTyrProCysAsnThrLeuGlnAl 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
PE: No. 6326469e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-426-509A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 528
Gaps: 4
Percent Identity: 71.023
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:US-08-594-447-1
                                                                                                                                                                                                                                                                                                                    Sequence 1, Patent No.
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                1572 GTCCACCGAGCCCCAGTACCAGCCCGGGGAGAAC 1605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1372 CTCACCACAAAGGGACGGGTGCCCTACCCTGGGATGGTGAACCGCGAGGT 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1072
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                 APPLICANT: Ron, Dorit
APPLICANT: Napolitano, Eugene W.
APPLICANT: Voronova, Anna F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1272 TGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGCC 1321
                                                                                                                                                                                                       TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH TITLE OF INVENTION: BLOCKTHE INTERACTION OF FYN WITH PKC-THETA, AND USES TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                   524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 ysPheThrIleLysSerAspValTrpSerPheGlyIleLeuLeuThrGlu
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                ZIP: 20006-1888
                                                                                             COUNTRY:
                                                                                                                          CITY: Washington
                                                                                                                                              STREET:
                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluArgProThrPheGluTyrLeuGlnSerPheLeuGluAspTyrPheTh 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCAAGTACCTGCGCCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGC 112:
                                                                                                                                                                                                                                                                                                                    , Application US/08594447 5776716
                                                                                                                                       2000 Pennsylvania Avenue, NW - Ste. 5500
                                                                                                  USA
                                                                                                                                                           MORRISON & FOERSTER
                                                                                                                                                                                          THEREOF: 75
 Version #1.30
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alignment_block:
US-09-444-711-1 x US-08-594-447-1
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; MOLECULE TYPE:
US-08-594-447-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 887-1500
TELEFAX: (202) 822-0168
TELEX: 90-4030 MRSMFOERSWSH
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 532 amino acids
TYPE: amino acid
                                                                                                                              359 ACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCC
                                                                                                                                                                                                                                                                     212 AC...ACCGTCACCTCCCCGCAGAGGGCGGGCCGGTGGCCGGTGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                         162 CGCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGG
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459 TGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGA 508
                                                                                                                                                                                                  85 ThrLeuPheValAlaLeuTyrAspTyr...AlaArgThrGluAspAspLe
                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                      71 erHisThrGlyThrLeuArgThrArgGlyGlyThr......GlyVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 hraspProThrProGlnHisTyrProSerPheGlyValThrSerIlePro
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                             AGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTT
                                                                                                AsnTyrAsnAsnPheHisAlaAlaGlyGlyGlnGlyLeuThr..... 62
                                                                                                                                                                     uSerPheHisLysGlyGluLysPheGlnIleLeuAsnSerSerGluGlyA
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                    /cgn2_6/ptodata/1/iaa/6B_COMB.pep:US-08-426-509A-11
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Sequence 11, Applicat Patent No. 6326469
GENERAL INFORMATION:

1, Application 6326469

US/08426509A

APPLICANT: APPLICANT: APPLICANT:

Ullrich, Axel Gishizsky, Mi) Sures, Irman (

Mikhail

Irman G.

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                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                   SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                               CITY: New York
                                    FILING DATE:
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Hofgarten Str. 2
Munchen 80539
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515 Galveston Drive
Redwood City, California 94063-4720
United States of America
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                             UMBER: PCT/US95/05008
24-APR-1995
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
459 TGGCAAGATCACCAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGA 508
                                          135
                                                                            409 AGCAACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTT 458
                                                                                                                     118
                                                                                                                                                         359 ACTGGTGGCTGGCCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCC
                                                                                                                                                                                                 101
                                                                                                                                                                                                                                    212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 CGCCCCCGCGGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                          85 ThrLeuPheValAlaLeuTyrAspTyrGluAlaArgThrGluAspAspLe 101
                                                                                                                                                                                                                                                                                                                                                     71 erHisThrGlyThrLeuArgThrArgGlyGlyThr......GlyVal 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 rGluGluArgAspGlySerLeuAsnGlnSerSerGlyTyrArgTyrGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 AsnTyrAsnAsnPheHisAlaAlaGlyGlyGlnGlyLeuThr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetGlyCysValGlnCysLysAspLysGluAlaThr....LysLeuTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                 spTrpTrpGluAlaArgSerLeuThrThrGlyGluThrGlyTyrIlePro 134
                                                                                                                                                                                               uSerPheHisLysGlyGluLysPheGlnIleLeuAsnSerSerGluGlyA 118
                                      SerAsnTyrValAlaProValAspSerIleGlnAlaGluGluTrpTyrPh
                                                                                                                                                                                                                                                                                                                                                                                           AC...ACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                 .....ValPheGlyGlyValAsnSerSerS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hrAspProThrProGlnHisTyrProSerPheGlyValThrSerIlePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 1932.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: PCT-US95-05008-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
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alignment_block: US-08-426-509A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
               813
                                                                                                                                                                         663
                                                                                                                                                                                                                                                                                                                                       513
                                                                                                                                                                                                                                                                                                                                                           114
                                                                                                                                                                                                                613 TACAAGATCCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGCAC
                                                                                                                                                                                                                                                                     563 GCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCAC
                                                                                                                                                                                                                                                                                                         313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 CCAGCAAGCCAGCCTCGGCCGACGGCCACCGCGCCCCAGCGCGCCTTC 162
                                         248
                                                                   763
                                                                                           231
                                                                                                                     713
                                                                                                                                               214
                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                   363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 CACCGTCACCTCCCCGCAGAGGGCCGGGCCCGCTGGCCGGTGGAGTGACCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 GCCCCCGCGCCGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 ysAlaArgProAlaSerSerPheAlaHisIleProAsnTyrSerAsnPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 AAGAGCAAGCCCAAGGATGCCAGCCAGCGGCGCCGCAGCCTGGAGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 pPheArgSerTyrGlyAlaAlaAspHisTyrGlyPro...AspProThrL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 CGAGAACGTGCACGGCGCTGGCGGGGGGGCGCTTTCCCCGCCTCGCAGACCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                           CCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCG 712
:|||||||||||:::|||:::||||| :::||| :::
| 1GlnPheAsnSerValGlnGluLeuValGlnHisTyrMetGluValAsnA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGA
                                      ACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAGGGACCTTCCTCGTGCGAGAAAGTGAGACCACGAAAGGTGCCTACT 562
                                                                                         spGlyLeuCysAsnLeuLeuIleAlaProCysThrIleMetLysProGln
                                                                                                                    ATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAG
                                                                                                                                                                                                  TyrLysIleArgLysLeuAspMetGlyGlyTyrTyrIleThrThrArgVa
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\silbs1/gcgdata/geneseq/geneseqp-emb1/AA1999
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Database sequences: 747574
Database length: 111073796
Search time (sec): 81.300000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query: US-09-444-7:
Query length: 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAB84661

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AAX4449

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:AAX37005

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AAX4451

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAB623778

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAB610302

/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAB84663
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-DB-A_Geneseq_032802 -OFMT-fastan -SUFFIX-n2p.rag -GAPOP=12.000
-GAPOR-4.500 -INMANCH-0.100 -LOOPCL-0.000 -LOOPCEXT-0.000
-OGAPOR-4.500 -QGAPEXT-0.050 -XGAPOR-10.000 -XGAPEXT-0.500
-FGAPOR-6.000 -FGAPEXT-7.000 -YGAPOR-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -STAFT-1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTPMT-pfs
-CRM-ext -HEAPSIZE-500 -MINLEN-0 -MALTEN-200000000
-SER-US09444711_eCGN1_10 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AAY44447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-444-711-1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /AA1993.DAT:AAR39706
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ID AAR39706 standard;
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:AAR15156
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:AAK850009
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The DNA encoding a portion or (more preferably) the entire pp60 c-src polypeptide (Given in AAQ46688) is used to transform endothel cells. Transformed cells produce increased amounts of pp60 c-src an have improved therapeutic properties. They migrate at faster rates than non-transformed counterparts; have an enhanced ability to inhibit the formation of thrombi and/or dissolve thrombi once they have formed and exhibit reduced mononuclear cell adhesion. They callso be used to improve the success of surgical procedures such as coronary angioplasty, heart bypass surgery, vessel graft and stent
                                                                                                                                                                                                                                                                                                               Genetically engineered endothelial cells - which exhibit enhanced cell migration, urokinase-type plasminogen activator activity, and reduced mononuclear cell adhesion and fibronectin prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human pp60 c-src protein
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                                                                                                                                                                                                                                                                  Disclosure; Page 75-77; 91pp; English.
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DB; AAR39705.
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US-09-444-711-1 x AAY44447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the wild-type chicken c-Src tyrosine kinase. This Src protein can be used to modulate angiogenesis. When the Src protein is inactivated, angiogenesis is inhibited while, when it is activated, angiogenesis is potentiated. The modified or variant Src be used to treat inflammatory diseases like, arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis, osteoporosis and cancer
                                                                                                                                                                                                                                                                                                                       101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACCGCCACCGCGGCCCC 150
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N-PSDB; AAZ29700.
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551	AAGGTGCCTACTGCCTCACTGTCTGACTTCGACAACGCCAAGGGCCT	000
181	ysGlyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLe	97
198	1 AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGGCGGCTTCTACAT 6 	550
651 214	CACCTCCCGCACCCAGTTCAACAGCCTGCAGC	700
701 231	1 CCAAACACGCCGATGGCCTGTGCCCACCGCCTCACCACCGTGTGCCCCACG 7 [750
751 248	TCCAAGCCGCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTCG 8	300
801 264	1 GGAGTCGCTGCAGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 8	350
. 281	1 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 9	900
901 298	1 AAGCCTGGCACGATGTCTCCAGAGGGCCTTCCTGCAGGAGGCCCAGGTCAT 9	
951 314	1 GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1 	1000
1001 331	1 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 1	1050 3 4 7
1051 348	1 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 1	1100
110: 36:	1 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA :	1150 ·
115 38	1 ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC :	1200 397
	1 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTC	1250 414
125 41	1 TGAGTACACGGCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 1	1300 431
130 43	1 CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 1	1350

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                            TGCCCTGCCCGCGGAGTCCCCGAGTCCCTGCACGACCTCATGTGCCAG
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ID AAY44449 standard; Pr
AC AAY44449;
XX 22-MAR-2000 (first e
XX 22-MAR-2000 (first e
XX Angiogenesis; tyrosin
KW Angiogenesis; tyrosin
KW chicken; mutant Src;
KW negative regulation;
KW rheumatoid arthritis;
XX Gallus sp.
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                                                                                                The present sequence is the mutant chicken c-Src tyrosine kinase, SrcA. This sequence has a point mutation, Y52FF, to activate c-Src. This site is involved in negative regulation by the kinase CSK. Phosphorylation of Tyr residue at 527 inactivates the protein. But in the mutated SrcA, the regulatory Tyr is replaced with Phe, thus constitutively activating the protein. This mutant Src protein can be used to modulate angiogenesis. When the Src protein is inactivated, angiogenesis is inhibited while, when it is activated, angiogenesis is inhibited while, when it is activated, angiogenesis like, arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis, osteoporosis and cancer associated disorders.

Note: This sequence is not found in the specification, but derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chicken; mutant Src; SrcA; point mutation; Y527F; phosphorylation; negative regulation; tyrosine; inflammatory disease; osteoporosis; rheumatoid arthritis; diabetic retinopathy; restenosis; cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page -; 80pp; English
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ID ABG23778 standard; Protein;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating
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                                                                                                                                                                                             Claim
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23-AUG-2000;
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medical imaging; diagnostic; genetic
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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polyperase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC control of the control of contr
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at ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000;
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TGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGG
                                               ACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG
                                spThrLeuGlnLysLeuValLysHisTyrThrGluHisAlaAspGlyLeu
                                                                                                                                                                       CCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCCCAGCAACTACGTG
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GGTACCACCAGGGTGGCCATCAAAACCCCTGAAGCCCTGGCACGATGTCTCCC
                                    alLysLeuGlyGlnGlyCysPheGlyGluValTrpMetGlyThrTrpAsn
                                                                                  TGCCACCGCCTCACCACCGTGTGCCCCACGTGCAAGCCGCAGACTCAGGG
                                                                                                                                                                                             ACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG
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alProSerSerTyrProAlaGlyLeuThrGlyGlyValThrIlePheVal
                                                           TCAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAAC
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yes1

protein. (first

23-SEP-1999

entry)

Human; yesl; diagnosis; neuropsychiatric disorder; BAD; bipolar affective disorder; attention deficit disorder; schizoaffective disorder; unipolar affective disorder; Huntington's disease; Parkinson's disease; manic-depres:

manic-depression

seq_documentation_block:

AAY24421 standard;

Protein;

543 æ

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:AAY24421

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                                                         efluargProThrPheGluTyrIleGlnSerPheLeuGluAspTyrPheT
                                                                                      GGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGGAGGACTACTTCA 1570
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                            CGTCCACCGAGCCCCAGTACCAGCCCGGGGAGAACCTC
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seq_documentation_block:
ID ABG23777 standard; Protein; 351
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WPI; 2001-639362/73
N-PSDB; AAS87964.
                                                                                                                        31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensions supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                             Novel human diagnostic protein #23768
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                                                    Drmanac RT,
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                                                                                                                                                                                                                    11-OCT-2001.
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                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                        (HYSE-) HYSEQ INC
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2000US-0649167.
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CC polynuclectides are also used in diagnostics as expressed sequence tags (for identifying expressed genes. (I) is useful in gene therapy techniques (C for identifying expressed genes. (I) a useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or committating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II), (I) and (II) are useful for treating (C imaging of sites expressing (II), (I) and (II) are useful for treating (C inspin) the polypeptide and polynucleotide sequences have applications in (id) and (iv) are useful for treating (II), (I) and (II) are useful for treating (I
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromc and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and
                                                                               ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID No
351 AA;
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alignment_block: alignment_scores: US-09-444-711-1 x ABG23777 Align seg 1/1 to: ABG23777 Percent Similarity: 100.000 Quality: 1867.00 Ratio: 5.319 from: 1 Gaps: 0
Percent Identity: 100.000 ţo:

556 GCCTACTGCCTCTCAGTGTCTGACTTCGACAACGCCAAGGGCCTCAACGT AlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeuAsnVa 17

17 CCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAA

706 CACGCCGATGGCCTGTGCCACCGCCTCACCACCGTGTGCCCACCGTCCAA

erArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaTyrTyrSerLys

50

34

51 HisAlaAspGlyLeuCysHisArgLeuThrThrValCysProThrSerLy 67

905

TGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCCAGGTCATGAAGA 955

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                               TGGCCGACTTTGGGCTGGCTCGTTGAAGACAATGAGTACACGGCG
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                                                                                                               Claim 1; Page 434-5; 438pp; English.
                                                                                                                                              Crystal of a protein-ligand complex for identifying kinase inhibitors, comprises a truncated lymphocyte kinase and a ligand, and diffracts X-rays to determine atomic coordinates at a resolution greater than 5
                                                                                                                                                                                                                                                                                                                                                            Human; lymphocyte kinase; protein
                                                                                                                                                                                                                                                                                                                                                                                Human lymphocyte kinase.
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The present invention relates to a crystal of a protein-ligand complex comprising a truncated lymphocyte kinase (lck) and a ligand. The crystal diffracts X-rays so that the atomic coordinates of the protein-ligand complex can be determined to a resolution of greater than 5.0 Angstroms. The truncated lck used in the present invention comprises the globular core of the corresponding full-length lck. The present sequence is the full-length human lck protein. The crystal of the present invention may be used to identify kinase inhibitors in screening assays, in drug screening and drug design processes, to design, select or test inhibitors of kinase enzymes, where the inhibitors are used as therapeutics for the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC The invention provides a novel method of altering the activity of the CC protein kinase A (PKA) signaling pathway in a cell that comprises CC altering the extent of phosphorylation of one or more PKA substrates, or CC kinase substrates downstream in the PKA signaling pathway. Pharmaceutical CC compositions containing a nucleic acid molecule that encodes a PKA CC substrate, or fragment, precursor or functionally equivalent variant, CC where the sequence is modified to alter its susceptibility to CC phosphorylation by PKA can be used for treating a disorder exhibiting CC abnormal PKA signaling activity, immunosuppressive disorders or CC proliferative diseases. They can be used for treating e.g. HIV CC infection, AIDS, common variable immunodeficiency or cancers. Conditions CC in which upregulation of the PKA pathway is required, such as autoimmune CC disease, e.g. systemic lupus erythematosus, may also be treated. The CC present sequence represents a PKA substrate, wherein the substrate is in CC the Src-family, preferably Lck, Fyn, Src, Yes, Fgr, Lyn, Hck Blk, Yrk, CC c-tkl, Fyk, Src-l or Src-2.
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                                                                                             rgIleLeuGluGlnSer...GlyGluTrpTrpLysAlaGlnSerLeuThr
                                                                                                                               AGATTGTCAACAACACGGAGGGAGACTGGTGGCTGGCCCACTCGCTCAGC
                                                                                                                                                                  rGluProSerHisAspGlyAspLeuGlyPheGluLysGlyGluProLeuA
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CATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAGTCAG
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                                  ThrGlyGlnGluGlyPheIleProPheAsnPheValAlaLysAlaAsnSe
                                                                  ACAGGACAGACAGCTACATCCCCAGCAACTACGTGGCGCCCCTCCGACTC
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                                                                                                                                                                                     GGCTCATTGAAGACAATGAGTACACGGCGCGCGAAGGTGCCAAATTCCCCC
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                                                                       IleLysTrpThrAlaProGluAlaIleAsnTyrGlyThrPheThrIleLy
                                                                                                                                                {\tt rgLeuIleGluAspAsnGluTyrThrAlaArgGluGlyAlaLysPhePro}
                                                                                                                                                                                                                                                                                                                                                                            hrIleAsnLysLeuLeuAspMetAlaAlaGlnIleAlaGluGlyMetAla
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                                                        TCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGCCGCTTCACC 1329
                            CTGCACGACCTCATGTGCCAGTGCTGGCGGAAGGAGCCTGAGGAGCGGCC 1529
LeuTyrSerIleMetLeuGlnCysTrpGlnGlnAspProGluGlnArgPr 472
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ID AAY49420 standard; PI
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AC AAY49420;
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13-MAR-2000 (first of the text of
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Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer; kinase substrate; immunosuppressive disorder; proliferative disease; HIV infection; AIDS; immunodeficiency; autoimmune disease; systemic lupus erythematosus; Src-family.

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                                CTTCGGGATCCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACC
                                                             {\tt ProGluAlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSe}
                                                                                                                              snGluTyrThrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAla
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; TOPOLOGY:
; MOLECULE TYP:
US-08-426-509A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:US-08-426-509A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application Patent No. 6326469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                        TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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                                                                                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York,
                                       STRANDEDNESS:
                                                                                                                                                                                NAME: COTUZZÍ, LAUTA A
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                          FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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               TYPE:
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No. 6326469e
                                                                          529 amino acids
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alignment_scores: Quality:

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Length: Gaps:

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seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: AAY4447

Protein;

3 4

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entry)

c-Src tyrosine kinase.

seq_documentation_block:
ID AAY44447 standard; PX
AC AAY44447;
XX
AC AAY44447;
XX
DT 22-MAR-2000 (first e
XX
Wild-type chicken c-:
XX
KW Angiogenesis; tyrosin
KW chicken; viral expres
KW diabetic retinopathy;
XX
PN W09961590-A1.
XX
PD 02-DEC-1999. Angiogenesis; tyrosine kinase; chicken; viral expression vectors inflammatory disease; retinopathy; expression vector; replication competent; isease; arthritis; rheumatoid arthritis; ri opathy; osteoporosis; cancer. Src; inhibition; activation; modul restenosis; modulate; riant Src;

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CCCCCXXX PTTXX DRXX
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The specification describes a method for modulating vascular permeability in a tissue suffering from a disease condition. The method comprises contacting the tissue with a pharmaceutical composition comprising tyrosine kinase protein Src, Yes or their mixtures or nucleic acid expressing them. The method is useful for modulating vascular permeability in tissues, including inflamed tissue, tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vascular permeability; tyrosine kinase protein; Src; Yes; stroke; myocardial infarction; restenosis; trauma; blood vessel; atherosc; diabetic retinopathy; inflammatory disease; infection; arthritis; adult respiratory distress syndrome; ARDS; rheumatoid arthritis; diabetic retinopathy; psoriasis; neovascular glaucoma; capillary proliferation; osteoporosis; cancer.
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                                                                                                                                           Modulating vascular permeability in tissues, including inflamed tissue tissues associated with stroke, myocardial infarction, by contacting the tissue with tyrosine kinase protein Src, Yes or their modified
                                                                                                                                                                                                                                                                                                   22-DEC-1999;
29-MAR-2000;
                                                                                                   Disclosure; Fig
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DB; AAH28357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             normal flow, tissues undergoing restenosis, psoriatic, retinal tissue and similar tissues. Pathologies which may be treated include include trauma to blood vessels, and other systemic pathological events such as atherosclerosis, diabetic retinopathy, inflammatory disease due to infection by microbial agents and arthritis. Other diseases which can be treated include adult respiratory distress syndrome (ARDS), rheumatoid arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma, capillary proliferation in atherosclerotic plaques and osteoporosis and cancer associated disorders such as solid tumours, solid tumour metastases, angiofibromas and hemangiomas. The present sequence represents chicken Src, and is used in the method of the invention.
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Gaps: 1
Percent Identity: 94.030
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alignment_block:
US-09-444-711-1 x AAY44449
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Ratio: 5.105
Percent Similarity: 97.201
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1 AGAACCTC 1608 1 luAsnLeu 533	CTTCCTGGAGGACTACTTCACGTCCACCGAGCCCCAGTACCAGCCCGGGG 16 	TGCTGGCGGAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGC 15 :::::::	TGCCCTGCCCGCCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAG 15	. TGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGA 14 	TTCGGGATCCTGCTGACCTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 14	CAGAAGCTGCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCC 13 	TGAGTACACGGCGGCGAGGTGCCAAATTCCCCATCAAGTGGACGGCTC 13 	1 CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTC	ACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC 12 	1 GGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATGA 11 	1 GACTTTCTCAAGGGGGAGACAGGCAAGTACCTGCGGCTGCCTCAGCTGGT 110 	1 AGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCTG 10 	GAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAG 1	1 AAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCAT 95	1 TGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG 90 	1 GGAGTCGCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCTGCTTTGGCGAGG 85
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seq_documentation_block:
ID AAR39705 standard; Protein; 533 AA
XX

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:AAR39705

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seq_documentation_block:
ID AAY44451 standard; P1
XX
AC AAY44451;
XX
DT 22-MAR-2000 (first 6
XX
XX
Mutant chicken c-Src
                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:AAY44451
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Synthetic.
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                                                                                                                                                                                                      Anglogenesis; tyrosine kinase; Src; inhibition; activation; modulate; chicken; mutant; Src(K295M); point mutation; tumour cell signalling; ATP binding; proliferation; kinase domain; inflammatory disease; canc osteoporosis; rheumatoid arthritis; diabetic retinopathy; restenosis.
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29-MAY-1998;
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                        28-MAY-1999;
                                                                           WO9961590-AJ
                                                                                                                             Misc-difference
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98US-0087220
                        99WO-US11780.
                                                                                                                          Location/Qualifiers
                                                                                                   /label= K295M
/note= "Wild :
                                                                                                                                                                                                                                                                                                                                                    Protein;
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yrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu

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alignment_block:
US-09-444-711-1 x AAY44451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the mutant chicken c-Src tyrosine kinase, Src(K295M). This sequence has a point mutation, K295M, in the kinase domain, which prevents ATP binding and also blocks kinase dependent Src functions related to vascular cell and tumour cell signalling and proliferation. This mutant Src(K295M) protein, can be used to modulate specifically, inhibit angiogenesis. When the Src protein is inactivated, angiogenesis is inhibited while, when it is activated, angiogenesis is potentiated. The mutant or variant Src can be used to treat inflammatory diseases like, arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis, osteoporosis and cancer associated disorders. Note: This sequence is not found in the specification, but derived from the sequence in Fig 2.
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               Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck; tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1; Hck signal transduction; human immunodeficiency virus; HIV infection;
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                                                                                                    tyrosine kinase Hck protein sequence SEQ
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214

ACCGTCACCTCCCCGCAGAGGGCGGGCCCGCTGGCCGGTGGAGTGACCAC SerHisAsnSerAsnThrProGlyIleArgGluAla..GlySerGluAsp

62 263 59

IleIleVal...

44

264

....ValAlaLeuTyrAspTyrGluAlaIleHisHisGluAspLeuSerP

63

heGlnLysGlyAspGlnMet...ValValLeuGluGluSerGlyGluTrp

93 363 78

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us-09-444-711-1 x AAB99332
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                                                                                                                                                                  Align seg 1/1 to:
                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                  to human tyrosine kinase Hck. Also described are: (1) nucleic acids encoding the protein and its derivatives; (2) recombinant vectors containing the nucleic acids; and (3) host cells transformed by the vectors and expressing the protein. HSB-1 has cytostatic activity, binds tyrosine kinase, enhances tumour necrosis factor alpha and promotes apoptosis. HSB-1 proteins are used for the elucidation of the mechanism of Hck signal transduction and of the role of Hck in human immunodeficiency virus (HIV) infection. They can be used for the treatment of infections and other diseases with which Hck is associated. They promote the anticancer activity of tumour necrosis factor alpha. The present sequence represents the human tyrosine kinase Hck protein, which is used in an example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis and for the elucidation of the mechanism of Hck signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New proteins which bind to human tyrosine kinase Hck for promotion
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164 CCCCCGCGGCCGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGGAC
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                                                                                                12 GlyGlyAsnThrPheSerLysThrGluThr.SerAlaSerProHisCysP
                                                                                                                                   82 GGCGGGGGCGCTTCCCCGCCTCGCAGACCCCCAGCAAGCCAG.....
                               roValTyrValProAspProThrSerThrIleLysProGly...ProAsn
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                                                          GCCCTCTATGGCCGCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGAT 1358
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                                                                                                                       CGGCGCGGCAAGGTGCCAAATTCCCCCATCAAGTGGACGGCTCCAGAAGCT 1308
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                                                                                                       hrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAlaProGluAla
                                             AlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSerPheGlyIl
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alignment_scores:
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APPLICANT: Ron, Dorit
APPLICANT: Voronova, Anna F.
APPLICANT: Napolitano, Eugene W.
TITLE OF INVENTION: METHODS TO IDENT
TITLE OF INVENTION: USING COGNATE IN
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                TELEX: 90-4030 MRSNFOERSWSH INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MUZAShige, Kate H.
REGISTRATION UNMBER: 29,959
REFERENCE/DOCKET NUMBER: 2255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1509
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COUNTRY: USA
TTD: 20006-1888
TTD: TEADABLE F
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 18-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483
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                                                                                                            FEATURE:
                                                                                                                             MOLECULE TYPE:
                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 2000 Peni
CITY: Washington
                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProGlnAspCysProIleSerLeuHisGluLeuMetIleHisCysTrpLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGGAGCCTGAGGAGCGGCCCACCTTCGAGTACCTGCAGGCCTTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/1aa/5B_COMB.pep:US-08-665-647-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Application US/08665647 5935803
                                                                                                                                                                                               532 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: MORRISON & FOERSTER 2000 Pennsylvania Avenue,
                                                                         CDS
1..1002
                                                                                                                                               linear
                                                                                                                             peptide
                                                                                                                                                              single
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THE INTERACTION OF PKC-THETA
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Quality: Ratio: Percent Similarity:

1944.00 4.208 84.000

Gaps: Percent Identity:

68.545

Length:

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TOPOLOGY: unknown;
MOLECULE TYPE: No. (
US-08-426-509A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-08-426-509A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-444-711-1 x US-08-426-509A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUIA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212.790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                     162 CGCCCCGCGGCCGAGCCCAAGCTGTTCGGAGGCTTCAACTCCTCGG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                212 AC...ACCGTCACCTCCCCGCAGAGGGCCGGGCCGCTGGCCGGTGGAGTG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NO
TITLE OF INVENTION: TY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
     71
                                                                                                                                        49 AsnTyrAsnAsnPheHisAlaAlaGlyGlyGlnGlyLeuThr..... 62
                                                                                                                                                                                                         32 hrAspProThrProGlnHisTyrProSerPheGlyValThrSerIlePro 48
                                                                                                                                                                                                                                                                              15 rGluGluArgAspGlySerLeuAsnGlnSerSerGlyTyrArgTyrGlyT 32
                                                                                                                                                                                                                                                                                                                 51 CCTGGAGCCCGCGAGAACGTGCACGGCGCTGGCGGGGGGGCGCTTTCCCCG 100
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/426,509A FILING DATE: 21-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                  1 MetGlyCysValGlnCysLysAspLysGluAlaThr....LysLeuTh 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/232,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
erHisThrGlyThrLeuArgThrArgGlyGlyThr......GlyVal 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New York,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 6326469e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30,742
ER: 7683-0074-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                         to: 537
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6
67.812
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259 85		01
309	GAGCGGCTCCAGATTGTCAACAAC :::::: ::: ::: GluLysPheGlnIleLeuAsnSer	358
359 118	CCACTCGCTCAGCACAGGACAGACAC ::: ::: aArgSerLeuThrThrGlyGluThrC	108 134
409 135	CAACTAĊGTGGCGCCCTCCGACTCCATÇCAGGCTGAGGAGTG ASNTYTVALALAPTOVALASPSETILEGLNALAGLUGLUTY	158 151
459 151	CAGAGCGGTTACTGCTCAATGC :: ::: laGluargGlnLeuLeuSerPh	80
168	ACCCGAGAGGGACCTTCCTCCTGCGAGAAAGTGAGACCACGAAAGGTGCC 5	558 L84
185	CCAAGGGCCT	508 201
609 201	GCACTACAAGATCCGCAAGCTGGACAGCGGCGGCGTTCTACATCACCTCCC 6	558 218
659 218	GCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACAC 7	
709 [.] 235	Va::	758 251
759 251	GCAGACTCAGGGCCTGGCCAAGGATGCCTGGGAGATCCCTC 7 :::	799
800 268	CTGGAGGTCAAGCT 	349
850 285	GTGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCT 8	399
301	GAAGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCA 9	118
950 318	TGAAGAAGCTGAGGCATGACAAGCTGGTGCAGTTGTATGCTGTGGTTTCA 9	34
1000 335	GAGGAGCCCATTTACATCGTCACGGAGTACATGAGCAAGGGGAGTTTGCT 1 	L049 851
1050 351	ACAGGCAAGTA ::: GluGlyArgAl	.099
1100 368	CTGCTCAGATCGCCTCAGGCATGGCGTACGTGGAGCGGATG 1 ::: ::: :::	149

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alignment_block: us-08-426-509A-14
                                                                                                                                             alignment_scores:
Quality: 2123.50
Ratio: 4.480
Percent Similarity: 86.813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
   Sequence 14, Application US/08426509A
   Patent No. 6326469
                                                                                                                                                                                                                                                              ; TOPOLOGY: unknown; MOLECULE TYPE: No. 6326469e US-08-426-509A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/laa/6B_COMB.pep:US-08-426-509A-14
                                                       Align seg 1/1 to: US-08-426-509A-14 from: 1 to: 543
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: COTUZZI, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-0074-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-99-9990
TELEPHONE: 212-99-9741
TELEX: 66141 PENNIE
NFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1601 AGAACCTC 1608
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 543 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ullrich,, Axel
APPLICANT: Gishizsky,, Mikhail
APPLICANT: Sures,, Irman G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                531 luAsnLeu 533
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TILE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TILE OF INVENTION: TYROSINE KINASES
1 ATGGGTAGCAAGAGCAAGCCC...AAGGATGCCAGCCAGCCGCCCG
                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York, STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                               Length:
Gaps:
Percent Identity:
                                                                                                                                             74.542
                                                                                                                                                                                     546
                     47
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920	871 GGTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCC	
297	lLysLeuGlyGlnGlyCysPheGlyGluValTrpMetGlyThrTrpAs	
870	AAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGA	
820 281	771 CCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGG	
770 264	721 TGCCACCGCCTCACCACGTGTGCCCCACGTCCAAGCCGCAGACTCAGGG :::	
42	::::: :::: ::: :::::	
720	CAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCT	
670 231	621 CCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCA ::: ::: ::: :::	
620 214	571 GTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGAT ::: ::: :::	
9		
181	yArgLysAspAlagiuArgLeuLeuLeuAsnProGlyAsnGinArgGly	
Ń	1 CAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAAACCCGAGAGAGG	
470 164	421 GCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCAC :::	
420 147	371 CCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCCCAGCAACTACGTG ::: :::: :::::	
370 131	321 AGGCGAGCGGCTCCAGATTGTCAACAACACGGAGGAGACTGGTGGCTGG 	
320 114	1 GCCCTCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAG ::: AlaLeuTyrAspTyrGluAlaArgThrThrGluAspLeuSerPheLys	
270 97	GCAGAGGGC ::: rSerTyrPr	
1 H	4 ySerSerGlyValThrProPheGlyGlyAlaSerSerSerPheSerVal	
220	AAGCTGTTCGGAGGCTTCAACTCCTCGGACACCGTC	
183 64	CGCGGCCTTCGCCCC:::: ::: aValAsnPheSerSe	
47	ThrThrValSerProCysProSerSerSerAla	
141	TTCCCCGCCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGG	
34	17 gProGluAsnThrProGluProValSerThrSerValSerHisTyrGlyA	
17	1 MetGlyCysIleLysSerLysGluAsnLysSerProAlaIleLysTyrA	

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1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321
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                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCAAGTACCTGCGGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCG 1120
                                                                                                                                                                          GGTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysHisLysLeuThrThrValCysProThrValLysProGlnThrGlnG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spThrLeuGlnLysLeuValLysHisTyrThrGluHisAlaAspGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YArgLysAspAlaGluArgLeuLeuLeuAsnProGlyAsnGlnArgGlyI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGCCCTCCGACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCAC 470
CGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAAGTGGCCGA
                                                                                                                                                                                                                                                                                                                                    AGAGGCCTTCCTGCAGGAGGCCCCAGGTCATGAAGAAGCTGAGGCATGAGA
                                                                                                                                                                                                                                                                                                                                                                    GlyThrThrLysValAlaIleLysThrLeuLysProGlyThrMetMetPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGCCAAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCACCGCCTCACCACCGTGTGCCCCCACGTCCAAGCCGCAGACTCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGACGGGAGTCAGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCACTCGCTCAGCACAGGACAGACAGGCTACATCCCCAGCAACTACGTG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaLeuTyrAspTyrGluAlaArgThrThrGluAspLeuSerPheLysLy
                                                 laAspGlyMetAlaTyrIleGluArgMetAsnTyrIleHisArgAspLeu
                                                                                 CCTCAGGCATGGCGTACGTGGAGCGGATGAACTACGTCCACCGGGACCTT
                                                                                                               pGlyLysTyrLeuLysLeuProGlnLeuValAspMetAlaAlaGlnIleA
                                                                                                                                                                                                          ACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAGGGGGAGAC 1070
                                                                                                                                                                                                                                                                                                    oGluAlaPheLeuGlnGluAlaGlnIleMetLysLysLeuArgHisAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yLeuAlaLysAspAlaTrpGluIleProArgGluSerLeuArgLeuGluV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAGCCTGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGCAAGCTGGACAGCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleArgAspTrpAspGluIleArgGlyAspAsnValLysHisTyrLysIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGTCTGACTTCGACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaProAlaAspSerIleGlnAlaGluGluTrpTyrPheGlyLysMetGl
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08426509A Patent No. 6326469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Ullric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1521
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                                                                                                                                     APPLICATION NUMBER: US/01 FILING DATE: 21-APR-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414
                          REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION: 212-790-9090
                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     514
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gishizsky,, Mikhail APPLICANT: Sures,, Irman G.
TELEPHONE: 212-869-9741
                                                                          NAME: Coruzzi, Laura REGISTRATION NUMBER:
                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                   ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                IBM Compatible
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                                                                        30,742
                                                                                                                                         08/232,545
                                                           7683-0074-999
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524 rAlaThrGluProGlnTyrGlnProGlyAspAsn 535

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alignment_block:
US-09-444-711-1 x PCT-US95-05008-12
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Quality: 1949.00
Ratio: 4.350
Percent Similarity: 84.848
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                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown ; ~ MOLECULE TYPE: protein PCT-US95-05008-12
                                                                                                                                                                Align seg 1/1 to: PCT-US95-05008-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Munchen 8
APPLICANT: Germany
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION UMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2: CORRESPONDENCE ADDRESS:
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                                                                                                                     24 aHisProProSerGlnTyrAspProAspProThrGlnLeuSerGlyAlaP 41
                                    93 TTTCCCCGCCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACGGC.... 138
                                                                              |||::::::: ||| ||| |||
| 6 GluLysIleSerGlyLysGlyGlnGlyGlySerGlyThrGlyThrProAl 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: un)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US95/05008 FILING DATE: 24-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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New York
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Redwood City, California 94063-4720
United States of America
Wissenschaften E.V.
Hofgarten Str. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugen, Inc
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                                                                                                                                                                                                                                                                         Percent Identity: 71.023
                                                                                                                                                                     from: 1
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139	CACCGCGGCCCCAGCGCGGGCCTTCGCCCCCGCGGGCCGCCGAGCCC 1	; B
184	AGCTGTTCGGAGGCTTCAACTCCTCGGACACCGTCACCTCCCCGCA	
58	 ProGlyPheTyrProCysAsnTh	4
231 74	GAGGGCGGGCCCGCTGGCCGGTGGACTGACCACCTTTGTGGCCCTCTATG 2 :::::::: ::: ::: :::	16
281 91	Fe C 3	330 107
331	CTCCAGATTGTCAACAACAACGGAGGAGACTGGTGGCTGGC	380
381	AGCACAGGACAGACAGCTACATCCCCAAGCAACTACGTGGCGCCCTCCG	w
124	ä-	141
431 141	ACTCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAG 4	180 157
481 158	TCAGAGCGGTTACTGCTCAATGCAGAGAGAACCCGAGAGGGACCTTCCTCGT 5 :::	530 174
531 174	GCGAGAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCAGTGTCTGACT :	580 191
581 191	TCGACAACGCCAAGGGCCTCAACGTGAAGGATACAAGATCCGCAAGCTG (:: :::	630 207
631 208	GACAGCGGCGGCTTCTACATCACCTCCCGCACCCAGTTCAACAGCCTGCA (:::::::::	680 224
681 224	GCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTGTGCCACCGCC	730 241
731 241	TCACCACCGTGTGCCCCACGTCCAAGCCGCAGACTCAGGGCCTGGCC	777 257
778 258	AAGGATGCCTGGGAGATCCCTCGGGAGTCGCTGCGGCTGGAAGT	821 274
822 274	CAAGCTGGGCCAGGGCTGCTTTGGCGAGGTGTGGATGGGGACCTGGAACG	871 291
872 291	GTACCACCAGGGTGGCCATCAAAACCCTGAAGCCTGGCACGATGTCTCCA ::: :::	921 307
922 308	GAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTGAGGCATGAGAA ::: ::: ::: GluAlaPheLeuGluGluAlaGInIleMetLysATgLeuATgHisAspLy	971 324
972 324	GCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTCA	102 341

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alignment_scores:
Quality: 2834.00
Ratio: 5.287
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: PCT-US95-05008-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 536 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                             nment_block:
09-444-711-1 x PCT-US95-05008-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAUTA A.
REGISTRATION UNMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEPHAX: (212)869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOT TITLE OF INVENTION: K11
NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                         151
                                                                                                                                                101 CCTCGCAGACCCCCAGCAAGCCAGCCTCGGCCGACCGGCCACCGCGCCCC 150
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51
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                                                                                                              34
                                                                                                                                                                                      17 rLeuGluProAlaGluAsnValHisGlyAlaGlyGlyGlyAlaPheProA
                                                                                                                                                                                                                           PPLICANT:
                                                                                                                                                                                                                                                                                DDRESSEE:
                                                                                                           MetGlySerAsnLysSerLysProLysAspAlaSerGlnArgArgArgSe 17
                                   AGCGCGGCCTTCGCCCCCGCGGCCCGAGCCCAAGCTGTTCGGAGGCTT 200
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Hofgarten Str. 2
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Gaps: 0
Percent Identity: 100.000
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1101 GGACATGGC	1051 GACTTTCTC 351 AspPheLeu	1001 AGGAGCCCA 334 luGluProI	951 GAAGAAGCT 317 tLysLysLe	901 AAGCCTGGC 301 LysproGly	851 TGTGGATGG 284 alTrpMetG	801 GGAGTCGCT 267 gGluSerLe	751 TCCAAGCCG 251 SerLysPrc	701 CCAAACACG 234 erLysHisA	651 CACCTCCCG 217 eThrSerAr	601 AACGTGAAG 201 AsnValLys	551 AAGGTGCCT 184 ysGlyAlaT	501 TGCAGAGAA 167 nalaGluas	451 TGGTATTTT 151 TrpTyrPhe	401 ACATCCCCA 134 yrilePros	351 GGAGGGAGA 117 rGluGlyAs	301 AČAGACCTG 101 ThraspLeu	251 GTGGAGTGA 84 lyGlyValT	 67 eAsnSerSe
TGCTCAGATCGCCTCAGGCA	AAGGGGGAGACAGGCAAGTA LysGlyGluThrGlyLysTy	TTTACATCGTCACGGAGTAC eTyrileValThrGluTyr	GAGGCATGAGAAGCTGGTGC 	ACGATGTCTCCAGAGGCCTT 	GGACCTGGAACGGTACCACC 	GCGGCTGGAGGTCAAGCTGG 	CAGACTCAGGGCCTGGCCAA 	CCGATGGCCTGTGCCACCGC 	CACCCAGTTCAACAGCCTGC 	CAAGCT gLysLe	ACTGCCTCTCAGTGTCTGAC 	.CCCGAGAGGGACCTTCCTCG 	GGCAAGATCACCAGACGGGA 	GCAACTACGTGGCGCCCTCC 	CTGGTGGCTGGCCCACTCGC 	TCCTTCAAGAAAGGCGAGCG 	CCACCTTTGTGGCCCTCTAT	
TGGCGTACGTGGAGCGGATGA	CCTGCGGCTGCCTCAGCTGGT rLeuArgLeuProGlnLeuVa	ATGAGCAAGGGGAGTTTGCTG 	AGTTGTATGCTGTGGTTTCAG 	CCTGCAGGAGGCCCAGGTCAT 	AGGGTGGCCATCAAAACCCTG 	GCCAGGGCTGCTTTGGCGAGG 	GGATGCCTGGGAGATCCCTCG 	CTCACCACCGTGTGCCCCACG 	AGCAGCTGGTGGCCTACTA 	GGACAGCGGCGGCTTCTACAT 	TTCGACAACGCCAAGGGCCTC 	TGCGAGAAAGTGAGACCACGA 	.GTCAGAGCGGTTACTGCTCAA 	GACTCCATCCAGGCTGAGGAG 	TCAGCACAGGACAGACAGCT 	GCTCCAGATTGTCAACAACAC 	GACTATGAGTCTAGGACGGAG 	
1150	1100	1050	1000	950	300.	284	267	750 250	700	650 · 217	200	184	167	450 150	400 134	350 117	300 100	8 4

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RESULT 14
US-09-228-603A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Weinstein, Daniel C.
TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 base pairs
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                               HYPOTHETICAL: FEATURE:
                                                                                                                                                                                                                    TELEPHONE: 201-487-5800
                                                                   MOLECULE TYPE:
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NAME/KEY:
                                                                                                                                                                                                                                                     NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-217 N
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 12-JAN-1999 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    STRANDEDNESS:
                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                     TOPOLOGY:
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US-08-426-509A-5

Sequence 5, Application Patent No. 6326469 GENERAL INFORMATION:

US/08426509A

APPLICANT:

Ullrich,, Axel

APPLICANT: Gishizsky,, Mikhail
APPLICANT: Sures,, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Eumonous STREET: 1155 Avenue of the

Americas

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Best Local Similarity
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                tggcggaaggagcctgaggagcggcccaccttcgagtacctgcaggccttcctggaggac 1563
                                                                             taccggatgccctgcccgccggagtgtcccgagtccctgcacgacctcatgtgccagtgc 1503
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APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzai, Yalda
                                      TITLE OF INVENTION: Protein Kinase Homologs
FILE REFERENCE: PF-0614 US
CURRENT APPLICATION UNMBER: US/09/173,581A
CURRENT FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 1574
                                                                                                                                                                                                                      "SENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer
                                                                                                                                             APPLICANT: Lu, Aina
                                                                                                                                                                                                                                                                         'quence 12, Appli
tent No. 6013455
      ORGANISM: HOMO FEATURE: -
                             TYPE: DNA
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                      APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Hillman, Jennifer L
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorgone, Gina
APPLICANT: Azimzai, Yalda
APPLICANT: Lu, Aina
                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                      Sequence 12, Application Patent No. 6264947
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Best Local Similarity
TITLE OF INVENTION: Protein FILE REFERENCE: pr-0614 US
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Pred. No. 8.
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Mismatches 198;
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Indels
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equence 1, Application Patent No. 5952213
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                          APPLICANT: Hemmati-Brivanlou, Ali
APPLICANT: Weinstein, Daniel C.
TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
A+h Floor
                                                                                                         STATE: N
COUNTRY:
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; LOCATION:
US-09-006-675-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-217
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                                                                        CACACTCGATGATGGAGGTTTCTTCATTTCTACACGGATCCCTTTTCCTTTGCCAGA
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22; Conservative
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Pred. No. 5.2e
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APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Edentically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Act
                  CORRESPONDENCE ADDRESS:
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NAME: Klee, Maurice M.

REGISTRATION NUMBER: 30,399

REGISTRATION NUMBER: LB-1(

TELECOMUNICATION INFORMATION:

TELEPHONE: (203) 255 1400

TELEPHONE: (203) 254 1101

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1602 base pairs
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 1373; Conserv
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ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the
TITLE: Gene and the Mechanism for Gener
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: Doub
TOPOLOGY: Linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 in
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DATE: March, 1983
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                                                       ACAGCAGCCCCGACACGCACCCCCAGCCGCTCCTTTGGGACCGTGGCCACCGAG
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                                                                                                                              Connecticut: USA
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85.2%;
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Pred. No. 5.9e-238;
0; Mismatches 229;
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RESULT 3 US-07-820-011A-1

Sequence 1, Application Patent No. 5336615 GENERAL INFORMATION:

APPLICANT:

NUMBER OF SEQUENCES:

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US-07-820-011A-3
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Best Local Similarity 99.5
Matches 1610; Conservative
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DATE: May, 1985
PUBLICATION INFORMATION:
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481 tcagagcggttactgctcaatgcagagaacccgagagggaccttcctcgtgcgagaaagt 540
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AUTHORS:
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PAGES:
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                                                                tggtggctggcccactcgctcagcacaggacaggctacatccccagcaactacgtg 420
                                                                                                          CCAGCCTCGGCCGACGGCCACCGCGGCCCAGCGCCGTTCGCCCCCGCGGCCGAG: 180
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May, 1987
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Human Cellular src Gene:

Nucleotide Sequence and Derived Amino
Acid Sequence of the Region Coding for
the Carboxy-Terminal Two-Thirds of
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Fujita, Donald J.
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Gibbs, Carol P.
Arthur, Richard R.
Anderson, Stephen K.
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Kung, Hsing-Jien
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4.4	aagggacgggtgccctaccctgggatggtgaaccgcgaggtgcttggaccaggtgttggagcgg	1381	P 9	
1380	GCTTCACCATCAAGTCGGACGTGTGGTCCTTCGGGATCCTGCTGACTGA		В	
1380	ogcttcaccatcaagtcggacgtgtgggtccttcggggatcctgctgactga	1321	Qy	
1320	GCGCGGCAAGGTGCCAAATTCCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGC	1261	뮍	
1320	cgcggcaaggtgccaaattccccatcaagtggacggctccagaagctgccctctatgg	1261	Qy	
1260	CTGGTGTGCAAAGTGGCCGACTTTGGGCTGGCTCGGCTC	1201	Db	
1260	tggtgtgcaaagtggccgactttgggctggctcggctcattgaagacaatgagtacac	1201	Qy	
1200	GAGCGGATGAACTACGTCCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAAC	1141	рь	
1200	aycyyatyaactacytccaccyyyaccttcgtycayccaacatcctyytyygayaya	1141	Qy	
1140	CTGCGGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACGTG	1081	Дb	
1140	tycyyctycctcayctyytyyacatyyctyctcayatcycctcayycatyycytacyt	1081	Qy	
1080	ACGGAGTACATGAGCAAGGGGAGTTTGCTGGACTTTCTCAAGGGGGAGACACGGCAAGTAC	1021	рь	
1080	cggagtacatgagcaaggggagtttgctggactttctcaagggggagacaggcaagta	1021	Ωу	
1020	AGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCCATTTACATCGTC	961	Db.	
1020	ggcatgagaagctggtgcagttgtatgctgtggtttcagaggagcccatttacatcg	961	Qy	
960	AGCCTGGCACGATGTCTCCAGAGGCCTTCCTGCAGGAGGCCCAGGTCATGAAGAAGCTG	901	Db	
960	agcctygcacgatgtctccagaggccttcctgcaggaggcccaggtcatgaagaagct	901	Qy	
900	TTTGGCGAGGTGTGGATGGGGACCTGGAACGGTACCACCAGGGTGGCCATCAAAACCCTG	841	DЬ	
900	ttggcgaggtgtggatggggacctggaacggtaccaccagggtggccatcaaaaccc	841	Qy	
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840	atqcctqqqaqatccctcqqqaqtcqctqcqqctqqaqqtcaaqctqqqccaqqqctq	781	VQ	
780	TGCCACCGCCTCACCACCGTGTGCCCCACGTCCAAGCCCGCAGACTCAGGGCCTGGCCAAG	721	Db	
780	gccaccgcctcaccaccgtgtgccccacgtccaagccgcagactcagggcctggccaa	721	Qy	
720	ACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAAACACGCCGATGGCCTG	661	Db	
720	cccagttcaacagcctgcagcagctggtggcctactactccaaacacgccgatggcct	661	Qγ	
660	AACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGGCGCTTCTACATCACCTCCCGC		당 5	
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Best Local S
Matches 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, c-ros, c-kit, c-met, c-trk, c-src, c-abl, bcr-abl, c-fgr and c-yes. The second oligonucleotide is specific for a nuclear oncogene of proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AMLL/MTGB, E2A/prl and ALL-1/AF-4. The composition Is used for treating cancer. The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.
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                                               ggagaaaatcttctgtgcaaaatagcagattttggtttagcaaggttaattgaagacaat
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malignanacy. The cellular immunogen comprises allogenic cells transfected with transgene construct comprising a transgene communog to target proto-oncogene and a strong promoter. The cellular immunog is useful for vaccinating a host against cancer by inserting the transgene construct into the body of the host for the expression of the transgene. The method of the invention is designed to target mutation-driven non-self determinants. The cellular immunogens induce reactivity for self-determinants in the over expressed product of tu

product of tumour

induce

immunogen

cellular immunogen for immunizing a host against the effects of product of a target proto-oncogene which is associated with a The present sequence represents a cognate transgene (CTG) which is rendered non-tumourigenic by deletion of amino acids 9-155. The CTG is used in the course of the invention. The specification describes

present sequence represents a cognate transgene (CTG) which

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
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                                                                                                                                                                                                                                                                                           The present invention describes a method for detecting a genetic mutation in the yeal gene for the diagnosis of a yeal mediated neuropsychiatric disorder in a human. The method comprises detecting the presence or absence of a genetic mutation in the yeal gene of the subject, where the genetic mutation is a substitution, insertion or a deletion and results in the production of a yeal protein having an amino acid sequence other than the wild-type yeal amino acid sequence and the presence of the genetic mutation identifies a subject that has or is at risk for developing a yeal mediated neuropsychiatric disorder. Compounds that bind to the yeal protein, alter the amount of the protein, or alter the activity of the yeal gene product, are useful for treating a yeal mediated neuropsychiatric disorder. The disorders include Huntington's disease, parkinson's disease, and especially bipolar-affected disorder (BAD) also known as bipolar mood disorder (BP) or manic-depressive illness. The method distinguishes neuropsychiatric disorders from neurological disorders, which enables more accurate evaluation and prescription of medical treatment. The present sequence represents the
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                                                          tttcatttaagaagggtgaaagatttcaaattaaccaatacggaaggagattggtggg
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955; Conser
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AAH18556

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Local Similarity nes 914; Conserv

Conservative

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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC cligonucleotide comprises at least 15 nucleotides; or (b) a combination CC complementary strand of a polynucleotide which comprises a 5'-end CC complementary strand of a polynucleotide which comprises a 5'-end CC complementary to comprises a 1 least 15 nucleotides; or (b) a combination CC complementary to comprises a 1 least 15 nucleotides and the combination of CC cligonucleotide comprises a 3'-end sequence, where the CC cligonucleotide comprises a 1 selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in GC cligonucleotide comprises are useful for synthesising polynucleotides, and cc in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the GC cligonucleotides of the abnormality of the proteins encoded by CC chapsing to the total and sequence and cc in the comprise of the abnormality of the proteins encoded by CC cligonucleotides. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs seasily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH18742 represent human cold sequences; AAB92446 to CC AAB9583 represent invano acid sequences; AAA9246 to AAH13632 cof the present invanion acid sequences; and AAH13629 to AAH13632 cof the present invanion acid sequences; and AAH13629 to AAH13632 cof the present invanion acid sequences; and AAH13639 to AAH13632 cof the present invanion acid sequences; and AAH13639 to AAH13632 cof the present invanion acid sequences; and AAH13639 to AAH13632 cof the present invanion acid sequences; and AAH13639 to AAH13632 cof the present invanion acid sequences; and AAH13639 to AAH13632 cof the present in
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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Best Local Similarity 85.5
Matches 1373; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disease; diabetic retinopathy;
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DB; AAY44447.
cccaagctgttcggaggcttcaactcctcggacaccgtcacctccccgcagaggggggg
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Pred. No. 1.4e-220;
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Sequence 2, Application PC/TUS9300445
GEBRAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madri, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthringer, Daniel J.
TITLE OF INVENTION: Genetically Er
TITLE OF INVENTION: Endothelial Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:PCT-US93-00445-2
                                                                            PILING DATE: 19930105

CLASSIFICATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 07/820,01

FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Klee, MAULICE M.
REGISTRATION UMBER: 30,399
REFERENCE/DOCKET NUMBER: ALX-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 533 amino acids
TYPE: AMINO ACTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1351 TTCGGGATCCTGACTGAGCTCACCACAAAGGGACGGGTGCCCTACCC 1400
MOLECULE TYPE:
HYPOTHETICAL: 1
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1401 TGGGATGGTGAACCGCGAGGTGCTGGACCAGGTGGAGCGGGGCTACCGGA 1450
                                    TYPE: AMINO ACID
TOPOLOGY: I.i.
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                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 760 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1951 Burr S
CITY: Fairfield
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: DELL 486/50
OPERATING SYSTEM: DOS 5.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                  No
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Complete Sequence
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The present sequence represents a human src family kinase (SFK)

designated laloo. Laloo plays a key role in the transformation of early

stage embryonic cells to mesodermal cells and is likely to be a

C proto-oncogene. SFK nucleic acids may be used to produce SFK proteins

and the functional domains of SFK, according to standard recombinant DNA

methodologies. The laloo SFK protein is involved in the transformation

of early stage embryonic cells into mesodermal cells and consequently

mutations its nucleic acids are major causes of early developmental

disorders. SFK is also thought to be a proto-oncogene involved in tumour

formation. Therefore, the nucleic acids may be used to study the

physiological and biochemical processes that cause early developmental

defects and tumour growth. The nucleic acids may be used as probe to

identify similar nucleic acids in biological samples and to quantify

clevels of expression. They may also be used to detect alterations within

those nucleic acids which may be related to disease. They may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sec_name:
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AAY29668 standard; Protein; 496
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Fig 1C; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for the detection of proto-oncogenes developmental defects in embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ08792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acids encoding vertebrate src-family kinases useful for the detection of proto-oncogenes and for diagnosing early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hemmati-Brivanlou A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:AAY29668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laloo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          src family kinase; SFK; proto-oncogene; gene therapy;
disorder; tumour formation; genetic vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0006675
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US-09-444-711-1 x AAY29668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1. to: AAY29668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used as primers in PCR to amplify and detect sequences encoding SFK. Additionally, the nucleic acids may be used in gene therapy protocols either as a genetic vaccine or as a transgene which is inserted into a patients genome to rectify inappropriate, or low levels of SFK expression in the patient. The SFK proteins encoded by the nucleic acids
583 GACAACGCCAAGGGCCTCAACGTGAAGCACTACAAGATCCGCAAGCTGGA
                                                             144
                                                                                                                                              127
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                                                                                                                                                                                                                             111
                                                                                                                                                                                                                                                             433 TCCATCCAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAGTC
                                                                                                                                                                                                                                                                                                                                                  383 GCACAGGACAGGCTACATCCCCAGCAACTACGTGGCGCCCTCCGAC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                 333 CCAGATTGTCAACAACACGGAGGGAGACTGGTGGCTGGCCCACTCGCTCA 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           may be used to assay for agents which modulate SFK expression and activity or as antigens in the production of antibodies against SFK. The proteins may also be administered to a patient to rectify inappropriate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                    GAGAAAGTGAGACCACGAAAGGTGCCTACTGCCTCTCAGTGTCTGACTTC
                                                                                                                                                                                   AGAGCGGTTACTGCTCAATGCAGAGAACCCGAGAGGGACCTTCCTCGTGC
                                                                                                                                        aGluArgGlnLeuLeuSerProValAsnLysSerGlyAlaPheMetIleA
                                                                                                                                                                                                                       SerLeuGluSerGluGluTrpTyrPheLysGlyMetSerArgLysGluAl
                                                                                                                                                                                                                                                                                                        erThrGlyGluGluGlyPheValProSerAsnTyrValAlaTyrPheAsn
                                                                                                                                                                                                                                                                                                                                                                                         u...LeuLeuLysLysGluSerGlyGluTrpTrpGluAlaCysLeuIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt TyrAspGlyValHisProGlyAspLeuThrPheArgLysGlyAspHisLe}
                                                         {\tt rgAspSerGluThrMetLysGlyCysPheSerLeuSerValArgAsp...}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is {\tt ProArgGluGluGluGluGluValValLeuLeuAlaLeuTyrAsp}
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Ratio: 3.549
milarity: 75.465
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